Frequentist network meta-analysis using the R package netmeta

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Outline

Starting point: Graph-theoretical methods for network meta-analysis

Statistical model

Multi-arm studies

Drawing the network

Ranking treatments

Inconsistency diagnostics

Summary
Networks are graphs

- **Nodes** are treatments
- **Edges** are comparisons between treatments, based on studies

‘Variances combine like electrical resistances’ (Bailey, 2007)

It is possible to apply methods from electrical network theory to network meta-analysis (Rücker, 2012)
Variances combine like electrical resistances

- **Connection in series** Variances in a chain of $n - 1$ independent comparisons of successive treatments $A, B, C, \ldots$ add:

  \[
  V_{A-E} = V_{A-B} + V_{B-C} + V_{C-D} + V_{D-E}
  \]

- **Parallel connection** For a pairwise meta-analysis with parallel comparisons, inverse variances add:

  \[
  \frac{1}{V(\bar{x})} = \sum_k \frac{1}{V_k}
  \]
## Terminology in meta-analysis and electrical networks

### Meta-analytic network
- **Treatments** \( i = 1, \ldots, n \) ➞ **Nodes** \( i = 1, \ldots, n \)
- **Existing comparisons** \( e = 1, \ldots, m \) ➞ **Edges** \( e = 1, \ldots, m \)
- **Variance** \( V_e \) ➞ **Resistance** \( R_e \)
- **Inverse variance weight** \( w_e = 1/V_e \) ➞ **Conductance** \( 1/R_e \)
- **Outcome of treatment** \( i \) ➞ **Potential at node** \( i \)
- **Treatment effect** \( i - j \) ➞ **Voltage at edge** \( i - j \)
- **Weighted treatment effect** \( i - j \) ➞ **Current flow at edge** \( i - j \)

### Electrical network
- **Nodes** \( i = 1, \ldots, n \)
- **Edges** \( e = 1, \ldots, m \)
- **Resistance** \( R_e \)
- **Conductance** \( 1/R_e \)
- **Potential at node** \( i \)
- **Voltage at edge** \( i - j \)
- **Current flow at edge** \( i - j \)

- **Ohm’s law** relates treatment effects and weights
- **Kirchhoff’s current law** says how to combine the observed effects
- **Kirchhoff’s potential law** guarantees **consistency** of the estimated treatment effects over closed circuits
  - Consistency means that the difference between two treatments is always the same, whatever (direct or indirect) path is chosen
Statistical model

Model

\[ \hat{\theta} = X\theta^{\text{treat}} + \epsilon, \quad \epsilon \sim \mathcal{N}(0, \Sigma), \]

where

- \( \hat{\theta} \) is a vector of \( m \) observed pairwise comparisons with known standard errors \( s = (s_1, s_2, \ldots, s_m) \)
- \( X \) is the \( m \times n \) design matrix defining the network structure
- \( \theta^{\text{treat}} \) a vector of length \( n \) (number of treatments)
- \( \Sigma \) is a diagonal matrix whose \( i^{\text{th}} \) entry is \( s_i^2 \).

Note:

- If there are \( K \) two-arm trials, \( \hat{\theta} \) has length \( K \)
- If there are also multi-arm trials, \( \hat{\theta} \) has length \( m \geq K \) with \( m \) denoting the total number of pairwise comparisons
Example network with \( n = 4 \) arms

- \( \theta^{treat} = (\theta_A, \theta_B, \theta_C, \theta_D)^T \)
- \( K = 5 \) studies each providing a single pairwise treatment comparison
- \( m = 5 \) pairwise treatment comparisons

Model:

\[
\begin{pmatrix}
\hat{\theta}_{AB}^1 \\
\hat{\theta}_{BC}^2 \\
\hat{\theta}_{CD}^3 \\
\hat{\theta}_{AD}^4 \\
\hat{\theta}_{BD}^5
\end{pmatrix}
= \begin{pmatrix}
1 & -1 & 0 & 0 \\
0 & 1 & -1 & 0 \\
0 & 0 & 1 & -1 \\
1 & 0 & 0 & -1 \\
0 & 1 & 0 & -1
\end{pmatrix}
\begin{pmatrix}
\theta_A \\
\theta_B \\
\theta_C \\
\theta_D
\end{pmatrix}
+ \begin{pmatrix}
\epsilon_1 \\
\epsilon_2 \\
\epsilon_3 \\
\epsilon_4 \\
\epsilon_5
\end{pmatrix}
= X\theta^{treat} + \epsilon
Estimation under the fixed effect model

- \( \mathbf{W} = \text{diag}(1/s_1^2, \ldots, 1/s_m^2) \) diagonal matrix (dimension \( m \times m \)) of inverse variance weights
- Network estimates \( \hat{\theta}^{nma} \) estimated by
  \[
  \hat{\theta}^{nma} = \mathbf{H}\hat{\theta}
  \]
  where \( \mathbf{H} = \mathbf{X}(\mathbf{X}^T\mathbf{WX})^+\mathbf{X}^T\mathbf{W} \) is known as the *hat matrix* in regression.
- Interpretation: The network estimates are weighted sums of the observed estimates with weights coming from the rows of \( \mathbf{H} \).
- Standard errors calculated from the variance-covariance matrix
  \[
  \text{Cov}(\hat{\theta}^{nma}) = \mathbf{X}(\mathbf{X}^T\mathbf{WX})^+\mathbf{X}^T
  \]
- Heterogeneity/inconsistency measured by generalised \( Q_{total} \) statistic
  \[
  Q_{total} = (\hat{\theta} - \hat{\theta}^{nma})^T\mathbf{W}(\hat{\theta} - \hat{\theta}^{nma})
  \]
  (Jackson et al., 2012; Rücker, 2012; Krahn et al., 2013)
Multi-arm studies: Need to account for correlation

- A study with $k$ arms contributes $\binom{k}{2}$ pairwise comparisons
- Note: These are correlated, as there are only $k$ treatments
  - $k - 1$ independent comparisons
  - $k - 1$ degrees of freedom ($df$)
- Example $k = 4$: $df = 3$
Adjustment for correlation within multi-arm studies

**Standard approach: Reduce dimension**
(Lu et al., 2011; Higgins et al., 2012; White et al., 2012; König et al., 2013)

- Based on standard regression methodology
- For each multi-arm study, choose a study-specific reference treatment
- Consider only comparisons to the reference treatment (‘basic parameters’)

**Alternative approach: Reduce weights**
(Rücker, 2012; Rücker and Schwarzer, 2014)

- Based on electrical network methodology
- For each multi-arm study, reduce all ‘conductances’ (weights) by specific factors that must be calculated
- Implemented in the R package **netmeta** (Rücker et al., 2016)
Comparison of the approaches

Standard approach

▶ Natural for statisticians with a background in regression analysis

Alternative approach

▶ Natural for scientists coming from graph theory and its applications

Given a four-arm study with six comparisons,
we may cut off three of six comparisons:
or reduce all weights by $1/2$ (in average):

\[
\begin{align*}
\text{Initial graph:} & \quad 1 & \quad 2 & \quad 3 & \quad 4 \\
\text{Reduction 1:} & \quad 1 & \quad 2 & \text{(3 cut off)} & \quad 4 \\
\text{Reduction 2:} & \quad 2 & \quad 1 & \text{(4 cut off)} & \quad 3 \\
\end{align*}
\]
Examples

1. **Diabetes data**
   Network of 10 diabetes treatments including 26 studies, where the outcome was HbA1c (measured as mean change or mean post treatment value) (Senn et al., 2013)

2. **Smoking cessation data**
   Network of four interventions for smoking cessation (binary outcome) (Higgins et al., 2012; Dias et al., 2013)

Both examples are part of R package netmeta
**How to use R package netmeta: Diabetes data**

```r
# Make R package netmeta available
install.packages("netmeta")
library(netmeta)

# Load diabetes data (Senn 2013), included in R package netmeta
data(Senn2013)
# Look at first 5 lines: data are in contrast-based format
head(Senn2013, 5)

## TE  seTE  treat1  treat2  studlab
## 1  -1.90  0.1414  metf  plac  DeFronzo1995
## 2   -0.82  0.0992  metf  plac  Lewin2007
## 3   -0.20  0.3579  metf  acar  Willms1999
## 4  -1.34  0.1435  rosi  plac  Davidson2007
## 5  -1.10  0.1141  rosi  plac  Wolffenbuttel1999

# Network meta-analysis of diabetes data
net1 <- netmeta(TE, seTE, treat1, treat2, studlab, data = Senn2013, sm = "MD",
comb.fixed=FALSE, comb.random=TRUE)
```
Summary output of diabetes data

# Summarize results

```r
summary(net1)
```

## Number of studies: k=26
## Number of treatments: n=10
## Number of pairwise comparisons: m=28

## Random effects model

## Treatment estimate (sm='MD'):

<table>
<thead>
<tr>
<th></th>
<th>acar</th>
<th>benf</th>
<th>metf</th>
<th>migl</th>
<th>piog</th>
<th>plac</th>
<th>rosi</th>
<th>sita</th>
</tr>
</thead>
<tbody>
<tr>
<td>acar</td>
<td>0.1106</td>
<td>-0.1106</td>
<td>0.2850</td>
<td>0.1079</td>
<td>0.2873</td>
<td>-0.8418</td>
<td>0.3917</td>
<td>-0.2718</td>
</tr>
<tr>
<td>benf</td>
<td>0.1106</td>
<td>0.3956</td>
<td>0.2186</td>
<td>0.3979</td>
<td>-0.7311</td>
<td>0.5023</td>
<td>-0.1611</td>
<td></td>
</tr>
<tr>
<td>metf</td>
<td>-0.2850</td>
<td>-0.3956</td>
<td>-0.1770</td>
<td>0.0023</td>
<td>-1.1268</td>
<td>0.1067</td>
<td>-0.5568</td>
<td></td>
</tr>
<tr>
<td>migl</td>
<td>-0.1079</td>
<td>-0.2186</td>
<td>0.1770</td>
<td>0.1794</td>
<td>-0.9497</td>
<td>0.2837</td>
<td>-0.3797</td>
<td></td>
</tr>
</tbody>
</table>

*** Output truncated ***

## Quantifying heterogeneity/inconsistency:

- $\tau^2 = 0.1087$; $I^2 = 81.4\%$

## Test of heterogeneity/inconsistency:

<table>
<thead>
<tr>
<th>Q d.f.</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>96.99</td>
<td>&lt; 0.0001</td>
</tr>
</tbody>
</table>
Forest plot of diabetes data

```r
# Look at result
forest(net1, ref = "plac",
       pooled = "random", digits=2,
       smlab = "Random effects model",
       xlab = "HbA1c difference",
       leftlabs = "Contrast to placebo")
```

<table>
<thead>
<tr>
<th>Contrast to placebo</th>
<th>Random Effects Model</th>
<th>MD</th>
<th>95%–CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>acar</td>
<td></td>
<td>-0.84</td>
<td>[-1.32; -0.36]</td>
</tr>
<tr>
<td>benf</td>
<td></td>
<td>-0.73</td>
<td>[-1.29; -0.17]</td>
</tr>
<tr>
<td>metf</td>
<td></td>
<td>-1.13</td>
<td>[-1.43; -0.82]</td>
</tr>
<tr>
<td>migl</td>
<td></td>
<td>-0.95</td>
<td>[-1.40; -0.50]</td>
</tr>
<tr>
<td>piog</td>
<td></td>
<td>-1.13</td>
<td>[-1.56; -0.70]</td>
</tr>
<tr>
<td>plac</td>
<td></td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>rosi</td>
<td></td>
<td>-1.23</td>
<td>[-1.48; -0.98]</td>
</tr>
<tr>
<td>sita</td>
<td></td>
<td>-0.57</td>
<td>[-1.26; 0.12]</td>
</tr>
<tr>
<td>sulf</td>
<td></td>
<td>-0.42</td>
<td>[-0.89; 0.06]</td>
</tr>
<tr>
<td>vild</td>
<td></td>
<td>-0.70</td>
<td>[-1.39; -0.01]</td>
</tr>
</tbody>
</table>
Smoking cessation data

# Load diabetes data (Senn 2013)
data(smokingcessation)

# Look at first lines: data are in arm-based format
head(smokingcessation)

## event1 n1 event2 n2 event3 n3 treat1 treat2 treat3
## 1 9 140 23 140 10 138 A C D
## 2 11 78 12 85 29 170 B C D
## 3 75 731 363 714 NA NA A C
## 4 2 106 9 205 NA NA A C
## 5 58 549 237 1561 NA NA A C
## 6 0 33 9 48 NA NA A C

# The first two trials are three-arm trials
Smoking cessation data

```r
# Transform data from arm-based format to contrast-based format
p2 <- pairwise(treat = list(treat1, treat2, treat3),
               event = list(event1, event2, event3),
               n = list(n1, n2, n3),
               data = smokingcessation, sm = "OR")

head(p2, 9)
```

<table>
<thead>
<tr>
<th>TE</th>
<th>seTE</th>
<th>studlab</th>
<th>treat1</th>
<th>treat2</th>
<th>event1</th>
<th>n1</th>
<th>event2</th>
<th>n2</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1.051293027</td>
<td>0.4132432</td>
<td>1</td>
<td>A</td>
<td>C</td>
<td>9</td>
<td>140</td>
<td>23</td>
<td>140</td>
</tr>
<tr>
<td>-0.128527575</td>
<td>0.4759803</td>
<td>1</td>
<td>A</td>
<td>D</td>
<td>9</td>
<td>140</td>
<td>10</td>
<td>138</td>
</tr>
<tr>
<td>0.922765452</td>
<td>0.3997972</td>
<td>1</td>
<td>C</td>
<td>D</td>
<td>23</td>
<td>140</td>
<td>10</td>
<td>138</td>
</tr>
<tr>
<td>-0.001244555</td>
<td>0.4504070</td>
<td>2</td>
<td>B</td>
<td>C</td>
<td>11</td>
<td>78</td>
<td>12</td>
<td>85</td>
</tr>
<tr>
<td>-0.225333286</td>
<td>0.3839393</td>
<td>2</td>
<td>B</td>
<td>D</td>
<td>11</td>
<td>78</td>
<td>29</td>
<td>170</td>
</tr>
<tr>
<td>-0.224088731</td>
<td>0.3722995</td>
<td>2</td>
<td>C</td>
<td>D</td>
<td>12</td>
<td>85</td>
<td>29</td>
<td>170</td>
</tr>
<tr>
<td>-2.202289286</td>
<td>0.1430439</td>
<td>3</td>
<td>A</td>
<td>C</td>
<td>75</td>
<td>731</td>
<td>363</td>
<td>714</td>
</tr>
<tr>
<td>-0.870353637</td>
<td>0.7910933</td>
<td>4</td>
<td>A</td>
<td>C</td>
<td>2</td>
<td>106</td>
<td>9</td>
<td>205</td>
</tr>
<tr>
<td>-0.415648522</td>
<td>0.1557329</td>
<td>5</td>
<td>A</td>
<td>C</td>
<td>58</td>
<td>549</td>
<td>237</td>
<td>1561</td>
</tr>
</tbody>
</table>

# Note the two three-arm studies 1 and 2, now each filling three data lines
Smoking cessation data

```r
net2 <- netmeta(TE, seTE, treat1, treat2, studlab, data = p2,
                comb.fixed = FALSE, comb.random = TRUE)

summary(net2)
```

```r
## Number of studies: k=24
## Number of treatments: n=4
## Number of pairwise comparisons: m=28

## Random effects model

## Treatment estimate (sm='OR'):
##       A      B      C      D
## A . 0.6595 0.4803 0.4056
## B 1.5162 . 0.7282 0.6150
## C 2.0822 1.3732 . 0.8446
## D 2.4653 1.6259 1.1840 .

*** (Output truncated) ***

## Quantifying heterogeneity/inconsistency:
## \(\tau^2 = 0.5989; \ I^2 = 88.6\%\)

## Test of heterogeneity/inconsistency:
##      Q d.f.  p.value
## 202.62 23 < 0.0001
```
Smoking cessation data

```r
# Define treatment names
tname <- c("No intervention","Self-help","Individual counselling","Group counselling")
# Produce network graph
# Transparent coloured areas correspond to three-arm studies
netgraph(net2, points=TRUE, cex.points=3, cex=1.25, labels=tname)
```
For network visualisation, use function **netgraph**

- Iteration method implemented in **netmeta**: Stress algorithm (Kamada and Kawai, 1989; Hu, 2012, related to multi-dimensional scaling)
- Various starting (also random) layouts available
- Iteration steps visible/printable, if desired
- Variable choice of scale, node size, line width, colours, highlighting
- Coloured polygons may represent multiarm studies (where transparent colours are available)
Drawing the network with netmeta: Diabetes data

![Network Diagram with Diabetes Data](image)
Drawing the network with netmeta: Diabetes data
Ranking treatments

- **Bayesian framework:**
  Derive ranking probabilities for each treatment from the posterior distributions

- Treatments may be ranked by the surface under the cumulative ranking curve (SUCRA) (Salanti et al., 2011)

- **Frequentist framework:**
  We introduced a quantity, called P-score, as an analogue to SUCRA (Rücker and Schwarzer, 2015)

- Example: Diabetes data
Surface under the cumulative ranking curve (SUCRA) for diabetes data (produced with WinBUGS and R)
Ranking treatments using P-scores: Diabetes data

- **P-scores** allow ranking the treatments on a continuous 0-1 scale
- Based on frequentist point estimates and standard errors
- Frequentist analogue to SUCRA (Rücker and Schwarzer, 2015)

```r
# Rank treatments
# Small values are "good" here (this is the default), otherwise "bad"
netrank(net1, small.values = "good")
```

```r
## P-score
## rosi 0.8934
## metf 0.7818
## piog 0.7746
## migl 0.6137
## acar 0.5203
## benf 0.4358
## vild 0.4232
## sita 0.3331
## sulf 0.2103
## plac 0.0139
```
Ranking treatments using P-scores: Diabetes data

Compare forest plot, point estimates, SUCRA values and P-scores

<table>
<thead>
<tr>
<th>Treatment</th>
<th>REM (frequentist analysis)</th>
<th>Frequentist</th>
<th>SUCRA</th>
<th>P-score</th>
</tr>
</thead>
<tbody>
<tr>
<td>rosiglitazone</td>
<td>-1.23</td>
<td>0.890</td>
<td>0.893</td>
<td></td>
</tr>
<tr>
<td>pioglitazone</td>
<td>-1.13</td>
<td>0.780</td>
<td>0.782</td>
<td></td>
</tr>
<tr>
<td>metformin</td>
<td>-1.13</td>
<td>0.773</td>
<td>0.775</td>
<td></td>
</tr>
<tr>
<td>miglitol</td>
<td>-0.95</td>
<td>0.620</td>
<td>0.614</td>
<td></td>
</tr>
<tr>
<td>acarbose</td>
<td>-0.84</td>
<td>0.520</td>
<td>0.520</td>
<td></td>
</tr>
<tr>
<td>benfluorex</td>
<td>-0.73</td>
<td>0.439</td>
<td>0.436</td>
<td></td>
</tr>
<tr>
<td>vildagliptin</td>
<td>-0.70</td>
<td>0.413</td>
<td>0.423</td>
<td></td>
</tr>
<tr>
<td>sitagliptin</td>
<td>-0.57</td>
<td>0.334</td>
<td>0.333</td>
<td></td>
</tr>
<tr>
<td>sulfonylurea</td>
<td>-0.42</td>
<td>0.213</td>
<td>0.210</td>
<td></td>
</tr>
<tr>
<td>placebo</td>
<td>0</td>
<td>0.018</td>
<td>0.014</td>
<td></td>
</tr>
</tbody>
</table>
Inconsistency diagnostics

Designs in network meta-analysis

- A design is each combination of treatments within a study in a network meta-analysis
  - Example: For three treatments $A, B, C$, the possible designs are $A : B$, $A : C$, $B : C$, $A : B : C$
  - For $n$ treatments the maximum number of designs is $2^n - n - 1$
  - Not all these need be present in a given network meta-analysis
  - In a pairwise meta-analysis, all trials have the same design $A : B$

- Clinical context
  - Example: Studies with design $A : C$ might differ to studies with design $A : B$ or $A : B : C$ in that they include patients who cannot be randomised to $B$
  - Heterogeneity between designs is plausible
Decomposition of the heterogeneity statistic

Total $Q$ statistic

$$Q_{total} = (\hat{\theta} - \hat{\theta}^{nma})^\top W (\hat{\theta} - \hat{\theta}^{nma})$$

Krahn et al. (2013):

- $Q$ can be decomposed into
  - a part coming from **within designs** (heterogeneity between studies of the same design)
  - a part coming from **between designs** (inconsistency between studies of different designs)
- $Q$ can be decomposed into parts coming from each design
- $Q$ can be decomposed into parts coming from each study
Decomposition of Q: Diabetes data

```r
# Decompose total Q statistics into parts from designs
decomp.design(net1)

## Q statistics to assess homogeneity / consistency
##
## Q  df  p.value
## Whole network 96.99 18  < 0.0001
## Within designs 74.46 11  < 0.0001
## Between designs 22.53  7   0.0021

## Design-specific decomposition of within-designs Q statistic
##
## Design  Q  df  p.value
## acar:plac 0.00  0 --
## acar:sulf 0.00  0 --
## benf:plac  4.38  1  0.0363
## metf:piog 0.00  0 --
## metf:plac 42.16  2  < 0.0001
## metf:rosi  0.19  1  0.6655
## metf:sulf 0.00  0 --
```

*** (Output truncated) ***

```r
## acar:metf:plac 0.00  0 --
```
## Decomposition of Q: Diabetes data

```r
# Decompose total Q statistics into parts from designs
decompl.design(net1)
```

### Between-designs Q statistic after detaching of single designs

<table>
<thead>
<tr>
<th>Detached design</th>
<th>Q</th>
<th>df</th>
<th>p.value</th>
</tr>
</thead>
<tbody>
<tr>
<td>acar:plac</td>
<td>22.44</td>
<td>6</td>
<td>0.001</td>
</tr>
<tr>
<td>acar:sulf</td>
<td>22.52</td>
<td>6</td>
<td>0.001</td>
</tr>
<tr>
<td>metf:piog</td>
<td>17.13</td>
<td>6</td>
<td>0.0088</td>
</tr>
<tr>
<td>metf:plac</td>
<td>22.07</td>
<td>6</td>
<td>0.0012</td>
</tr>
<tr>
<td>metf:rosi</td>
<td>22.52</td>
<td>6</td>
<td>0.001</td>
</tr>
<tr>
<td>metf:sulf</td>
<td>7.51</td>
<td>6</td>
<td>0.276</td>
</tr>
<tr>
<td>piog:plac</td>
<td>17.25</td>
<td>6</td>
<td>0.0084</td>
</tr>
<tr>
<td>piog:rosi</td>
<td>22.48</td>
<td>6</td>
<td>0.001</td>
</tr>
<tr>
<td>plac:rosi</td>
<td>16.29</td>
<td>6</td>
<td>0.0123</td>
</tr>
<tr>
<td>rosi:sulf</td>
<td>6.77</td>
<td>6</td>
<td>0.3425</td>
</tr>
<tr>
<td>acar:metf:plac</td>
<td>22.38</td>
<td>5</td>
<td>0.0004</td>
</tr>
</tbody>
</table>

Explanation: Detaching a design means relaxing the consistency assumption for this design. If Q decreases markedly after detaching a design (** added for the purpose of this talk), we conclude that this design contributed to between-design inconsistency. If Q does not decrease markedly, the design is not thought to contribute to between-design inconsistency.
Net heat plot (Krahn et al., 2013): Diabetes data

```
netheat(net1)
```
Net heat plot (Krahn et al., 2013)

- Areas of grey squares ■: indicate the contribution from the treatment comparison in the column to the treatment comparison in the row
- Colours on the diagonal represent the inconsistency contribution of the corresponding design (red means large)
- Colours on the off-diagonal associated with the change in inconsistency between direct and indirect evidence in a network estimate in the row after relaxing the consistency assumption for the effect of one design in the column
  - Blue indicates that the evidence of the design in the column supports the evidence in the row
  - Red indicates that the evidence of the design in the column contrasts to the evidence in the row
- Largest inconsistency contribution by the metf:sulf and rosi:sulf designs (red squares in top left corner)
Summary

R package **netmeta** provides

- flexible data entry (**pairwise**)
- fixed / random effects model (**netmeta**)
- appropriate incorporation of multi-arm trials
- forest plots (**forest**)
- network graphs (**netgraph**)
- ranking of treatments (**netrank**)
- inconsistency diagnostics (**decomp.design, netheat**)

Currently not available: Meta-regression

See book Schwarzer et al. (2015)
References


Appendix: A proof that SUCRA and P-score are the same

We assume the true probabilities as known. If $R(i) = k$ means that treatment $i$ has rank $k$, we have

$$P_{ij} = \sum_{k=1}^{n-1} \sum_{l=k+1}^{n} P(R(i) = k \land R(j) = l)$$

and

$$(n - 1)SUCRA(i) = \sum_{r=1}^{n-1} F(i, r) = \sum_{r=1}^{n-1} \sum_{k=1}^{r} P(i, k) = \sum_{k=1}^{n-1} \sum_{r=k}^{n-1} P(i, k) = \sum_{k=1}^{n-1} (n - k)P(i, k)$$

It follows

$$\sum_{j=1}^{n} P_{ij} = \sum_{j=1}^{n} \sum_{k=1}^{n-1} \sum_{l=k+1}^{n} P(R(i) = k \land R(j) = l) = \sum_{k=1}^{n-1} \sum_{l=k+1}^{n} \sum_{j=1}^{n} P(R(i) = k \land R(j) = l)$$

$$= \sum_{k=1}^{n-1} \sum_{l=k+1}^{n} P(i, k) = \sum_{k=1}^{n-1} (n - k)P(i, k) = (n - 1)SUCRA(i)$$

and thus

$$\bar{P}_i = \frac{1}{n - 1} \sum_{j=1}^{n} P_{ij} = SUCRA(i)$$

which is what we wanted to prove. Note: For $n > 2$, neither ranking probabilities $P(i, k)$ nor probabilities $P_{ij}$ can be uniquely determined from $\bar{P}_i$ or $SUCRA(i)$.